1600

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RAW SEQUENCE LISTING   DATE: 06/05/2003
PATENT APPLICATION: US/09/495,448A   TIME: 11:15:37

Input Set : A:\50111301_1.TXT
Output Set: N:\CRF4\06052003\I495448A.raw

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      3 <110> APPLICANT: LAU, Lester F.
      5 <120> TITLE OF INVENTION: EXTRACELLULAR MATRIX SIGNALLING MOLECULES
      7 <130> FILE REFERENCE: 28758/36072
C-->  9 <140> CURRENT APPLICATION NUMBER: US/09/495,448A
C--> 10 <141> CURRENT FILING DATE: 2000-01-31
     12 <150> PRIOR APPLICATION NUMBER: 09/142,569
     13 <151> PRIOR FILING DATE: 1999-04-02
     15 <150> PRIOR APPLICATION NUMBER: 60/013,958
     16 <151> PRIOR FILING DATE: 1996-03-15
     18 <160> NUMBER OF SEQ ID NOS: 34
     20 <170> SOFTWARE: PatentIn Ver. 2.0
     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 1480
     24 <212> TYPE: DNA
     25 <213> ORGANISM: Mus musculus
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     28 <221> NAME/KEY: CDS
     29 <222> LOCATION: (180)..(1316)
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     39 ctcgccggct tgttggttct gtgtcgccgc gctcgccccg gttcctcctg cgcgccaca 179
     41 atg agc tcc agc acc ttc agg acg ctc gct gtc gcc gtc acc ctt ctc 227
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     43  1               5                  10                  15
     45 cac ttg acc aga ctg gcg ctc tcc acc tgc ccc gcc gcc tgc cac tgc 275
     46 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
     47               20                  25                  30
     49 cct ctg gag gca ccc aag tgc gcc ccg gga gtc ggg ttg gtc cgg gac 323
     50 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
     51            35                  40                  45
     53 ggc tgc ggc tgc tgt aag gtc tgc gct aaa caa ctc aac gag gac tgc 371
     54 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
     55      50                  55                  60
     57 agc aaa act cag ccc tgc gac cac acc aag ggg ttg gaa tgc aat ttc 419
     58 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
     59 65                  70                  75                  80
     61 ggc gcc agc tcc acc gct ctg aaa ggg atc tgc aga gct cag tca gaa 467
     62 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
     63               85                  90                  95
     65 ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa agc 515
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 70 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
 71         115             120                 125
 73 ggc tgc att cct ctg tgt ccc caa gaa ctg tct ctc ccc aat ctg ggc   611
 74 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
 75         130             135                 140
 77 tgt ccc aac ccc cgg ctg gtg aaa gtc agc ggg cag tgc tgt gaa gag   659
 78 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
 79 145             150             155                 160
 81 tgg gtt tgt gat gaa gac agc att aag gac tcc ctg gac gac cag gat   707
 82 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
 83             165             170                 175
 85 gac ctc ctc gga ctc gat gcc tcg gag gtg gag tta acg aga aac aat   755
 86 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
 87         180             185                 190
 89 gag tta atc gca att gga aaa ggc agc tca ctg aag agg ctt cct gtc   803
 90 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
 91         195             200                 205
 93 ttt ggc acc gaa ccg cga gtt ctt ttc aac cct ctg cac gcc cat ggc   851
 94 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
 95         210             215                 220
 97 cag aaa tgc atc gtt cag acc acg tct tgg tcc cag tgc tcc aag agc   899
 98 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
 99 225             230             235                 240
101 tgc gga act ggc atc tcc aca cga gtt acc aat gac aac cca gag tgc   947
102 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
103             245             250                 255
105 cgc ctg gtg aaa gag acc cgg atc tgt gaa gtg cgt cct tgt gga caa   995
106 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
107         260             265                 270
109 cca gtg tac agc agc cta aaa aag ggc aag aaa tgc agc aag acc aag  1043
110 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
111         275             280                 285
113 aaa tcc cca gaa cca gtc aga ttt act tat gca gga tgc tcc agt gtc  1091
114 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
115         290             295                 300
117 aag aaa tac cgg ccc aaa tac tgc ggc tcc tgc gta gat ggc cgg tgc  1139
118 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
119 305             310             315                 320
121 tgc aca cct ctg cag acc aga act gtg aag atg cgg ttc cga tgc gaa  1187
122 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
123             325             330                 335
125 gat gga gag atg ttt tcc aag aat gtc atg atg atc cag tcc tgc aaa  1235
126 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
127             340             345                 350
129 tgt aac tac aac tgc ccg cat ccc aac gag gca tcg ttc cga ctg tac  1283
130 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
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133 agc cta ttc aat gac atc cac aag ttc agg gac taagtgcctc cagggttcct 1336
134 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
135     370              375
137 agtgtgggct ggacagagga gaagcgcaag catcatggag acgtgggtgg cggaggatg 1396
139 aatggtgcct tgctcattct tgagtagcat tagggtattt caaaactgcc aagggctga 1456
141 tgtggacgga cagcagcgca gccg                                    1480
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145 <211> LENGTH: 379
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154             20                  25                  30
156 Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
157         35                  40                  45
159 Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
160     50                  55                  60
162 Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
163  65                  70                  75                  80
165 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
166             85                  90                  95
168 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
169         100             105             110
171 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
172         115             120             125
174 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
175     130             135             140
177 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
178 145             150             155             160
180 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
181             165             170             175
183 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
184             180             185             190
186 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
187         195             200             205
189 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
190     210             215             220
192 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
193 225             230             235             240
195 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
196             245             250             255
198 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
199         260             265             270
201 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
202     275             280             285
204 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
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205     290                     295                     300
207 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
208 305                     310                     315                     320
210 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
211                     325                     330                     335
213 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
214             340                     345                     350
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232 <220> FEATURE:
233 <223> OTHER INFORMATION: Human cyr61 cDNA coding sequence
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240 aca atg agc tcc cgc atc gcc agg gcg ctc gcc tta gtc gtc acc ctt    168
241     Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
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245 Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
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248 tgc ccc ctg gag gcg ccc aag tgc gcg ccg gga gtc ggg ctg gtc cgg    264
249 Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
250             35                  40                  45
252 gac ggc tgc ggc tgc tgt aag gtc tgc gcc aag cag ctc aac gag gac    312
253 Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
254         50                  55                  60
256 tgc agc aaa acg cag ccc tgc gac cac acc aag ggg ctg gaa tgc aac    360
257 Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
258     65                  70                  75
260 ttc ggc gcc agc tcc acc gct ctg aag ggg atc tgc aga gct cag tca    408
261 Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
262 80                  85                  90                      95
264 gag ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa    456
265 Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
266             100                     105                     110
268 agt ttc cag ccc aac tgt caa cat cag tgc aca tgt att gat ggc gcc    504
269 Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
270             115                     120                     125
272 gtg ggc tgc att cct ctg tgt ccc caa gaa cta tct ctc ccc aac ttg    552
273 Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu
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281 Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln
282 160                 165                   170                   175
284 gac ggc ctc ctt ggc aag gag ctg gga ttc gat gcc tcc gag gtg gag   696
285 Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu
286                 180                 185                   190
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289 Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu
290                 195                 200                   205
292 aag cgg ctc cct gtt ttt gga atg gag cct cgc atc cta tac aac cct   792
293 Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro
294        210                 215                   220
296 tta caa ggc cag aaa tgt att gtt caa aca act tca tgg tcc cag tgc   840
297 Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys
298        225                 230                   235
300 tca aag acc tgt gga act ggt atc tcc aca cga gtt acc aat gac aac   888
301 Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
302 240                 245                   250                   255
304 cct gag tgc cgc ctt gtg aaa gaa acc cgg att tgt gag gtg cgg cct   936
305 Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro
306                 260                 265                   270
308 tgt gga cag cca gtg tac agc agc ctg aaa aag ggc aag aaa tgc agc   984
309 Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser
310                 275                 280                   285
312 aag acc aag aaa tcc ccc gaa cca gtc agg ttt act tac gct gga tgt   1032
313 Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys
314        290                 295                   300
316 ttg agt gtg aag aaa tac cgg ccc aag tac tgc ggt tcc tgc gtg gac   1080
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322 320                 325                   330                   335
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330                 355                 360                   365
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VERIFICATION SUMMARY   DATE: 06/05/2003
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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date